

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:09:42 ; Search time 52.57 Seconds

(without alignments)
133.774 Million cell updates/sec

Title: US-09-331-631a-22_COPY_25_84

Perfect score: 350

Sequence: 1 EDDNNHHHGKSGQCVRCR.....EKRDRSRHREADRSGEGSS 60

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	350	100.0	122	10	Q03863 zea mays (m
2	350	100.0	582	10	Q03865 zea mays (m
3	346	98.9	238	10	Q9SBE5 zea luxuria
4	346	98.9	238	10	Q9SBE5 zea luxuria
5	346	98.9	240	10	Q9SBE5 zea luxuria
6	346	98.9	540	10	Q03866 zea mays (m
7	342	97.7	238	10	Q03866 zea mays (m
8	342	97.7	238	10	Q03866 zea mays (m
9	342	97.7	238	10	Q03866 zea mays (m
10	342	97.7	240	10	Q03866 zea mays (m
11	342	97.7	240	10	Q03866 zea mays (m
12	342	97.7	240	10	Q03866 zea mays (m
13	342	97.7	407	10	Q03866 zea mays (m
14	342	97.7	238	10	Q03866 zea mays (m
15	340	97.1	240	10	Q03866 zea mays (m
16	338	96.6	238	10	Q03866 zea mays (m
17	337	96.3	236	10	Q03866 zea mays (m
18	334	95.4	242	10	Q03866 zea mays (m
19	334	95.4	242	10	Q03866 zea mays (m

20	331	94.6	239	10	Q9SBE1	Q9SBE1 zea mays su
21	325	92.9	239	10	Q03863	Q03863 zea mays su
22	320	91.4	236	10	Q03865	Q03865 zea mays su
23	303	86.6	236	10	Q03865	Q03865 zea mays su
24	279.5	79.9	246	10	Q03865	Q03865 zea mays su
25	270.5	77.3	242	10	Q03865	Q03865 zea mays su
26	256.5	73.3	242	10	Q03865	Q03865 zea mays su
27	129.5	27.9	637	10	Q03865	Q03865 zea mays su
28	97.5	27.9	393	10	Q03865	Q03865 zea mays su
29	96.5	27.6	1465	5	Q03865	Q03865 zea mays su
30	85	24.3	402	10	Q03865	Q03865 zea mays su
31	80.5	23.0	376	5	Q03865	Q03865 zea mays su
32	80.5	23.0	625	10	Q03865	Q03865 zea mays su
33	79.5	22.7	666	10	Q03865	Q03865 zea mays su
34	78	22.3	339	11	Q03865	Q03865 zea mays su
35	77.5	22.1	666	10	Q03865	Q03865 zea mays su
36	74	21.1	186	5	Q03865	Q03865 zea mays su
37	74	21.1	206	5	Q03865	Q03865 zea mays su
38	74	21.1	971	5	Q03865	Q03865 zea mays su
39	73.5	21.0	3080	5	Q03865	Q03865 zea mays su
40	73	20.9	598	5	Q03865	Q03865 zea mays su
41	72	20.6	292	10	Q03865	Q03865 zea mays su
42	72	20.6	704	5	Q03865	Q03865 zea mays su
43	71.5	20.4	143	5	Q03865	Q03865 zea mays su
44	71	20.3	603	6	Q03865	Q03865 zea mays su
45	70.5	20.1	757	5	Q03865	Q03865 zea mays su

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	122 AA.
ID Q03863			
AC Q03863;			
DT 01-NOV-1996 (TREMUREL. 01, Created)			
DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)			
DT 01-MAY-2000 (TREMUREL. 13, Last annotation update)			
DE GLBI-0 PROTEIN.			
GN GLBI-0.			
OS Zea mays (Maize).			
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.			
OC NCBI_TaxID=4577;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=92090707; PubMed=1752424;			
RA Belanger F.C., Kriz A.L.;			
RT "Molecular basis for allelic polymorphism of the maize Globulin-1			
RT gene.";			
RL Genetics 129:863-872(1991).			
DR EMBL: X59085; CAA41811.1;			
DR MENDEL: 14637; Zeama:1188;14637.			
SQ SEQUENCE 122 AA; 13902 MW; 9D03F64BFE9D6F2A CRC64;			
Query Match	100.0%;	Score 350;	DB 10;
Best Local Similarity	100.0%;	Pred. No. 3.4e-32;	Length 122;
Matches 60;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps 0;			
QY 1 EDDNNHHHGKSGQCVRCRCDPRWHDPRCLDQCREREKROERSRHADRSRGGSS 60			
DB 25 EDDNNHHHGKSGQCVRCRCDPRWHDPRCLDQCREREKROERSRHADRSRGGSS 84			
RESULT 2	PRELIMINARY:	PRT:	582 AA.
ID Q03865			
AC Q03865;			
DT 01-NOV-1996 (TREMUREL. 01, Created)			
DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)			
DT 01-OCT-2000 (TREMUREL. 15, Last annotation update)			
DE VICILIN-LIKE EMBRYO STORAGE PROTEIN.			

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GN  GUB1-L.
OS  Zea mays (maize).
OC  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC  Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX  NCBI_TaxId=4577;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=M64A.
RX  MEDLINE=92090707; PubMed=1752424;
RT  Belanger F.C., Kriz A.L.;
RT  "Molecular basis for allelic polymorphism of the maize globulin-1
RT  gene.";
RL  Genetics 129:863-872(1991).
DR  EMBL; X59083; CAA41809.1; -.
DR  HSSP; P50477; ICAU.
DR  MENDEL; 11234; Zeama:1188;11234.
DR  INTERPRO; IPR000901; -.
DR  INTERPRO; IPR001113; -.
DR  PFAM; PF00546; Seedstore_7s; 1.
DR  PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
DR  PRODOM; PD081059; -. 1.
KW  Seed storage protein.
SQ  SEQUENCE 582 AA; 66162 MW; 680D85FEC07C885 CRC64;
```

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Query Match          100.0%; Score 350; DB 10; Length 582;
Best Local Similarity 100.0%; Pred. No. 1.2e-31;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY  1 EDDNNHHHGHSKSGCVRCEDEPRMHPRCLEQCREEERERKQERSRHREADRSGEGSS 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB  25 EDDNNHHHGHSKSGCVRCEDEPRMHPRCLEQCREEERERKQERSRHREADRSGEGSS 84
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RESULT 3
ID  09SBE5          PRELIMINARY;      PRT;      238 AA.
AC  09SBE5;
DT  01-MAY-2000 (TREMBLrel. 13, Created)
DT  01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT  01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE  GLOBULIN-1 (FRAGMENT).
OS  Zea luxurians (Teosinte).
OC  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC  Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX  NCBI_TaxId=15945;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  Hilton H., Gaut B.S.;
RT  "Speciation and domestication in maize and its wild relatives:
RT  evidence from the globulin-1 gene.";
RL  Genetics 0:0-0(1998).
DR  EMBL; AF064231; AAC31474.1; -.
DR  HSSP; P50477; ICAU.
DR  INTERPRO; IPR000901; -.
DR  INTERPRO; IPR001113; -.
DR  PFAM; PF00546; Seedstore_7s; 1.
DR  PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
FT  NON_TER 238
SQ  SEQUENCE 238 AA; 27254 MW; FFA7BA7BA425D68 CRC64;
```

```
Query Match          98.9%; Score 346; DB 10; Length 238;
Best Local Similarity 98.3%; Pred. No. 1.6e-31;
Matches 59; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
OY  1 EDDNNHHHGHSKSGCVRCEDEPRMHPRCLEQCREEERERKQERSRHREADRSGEGSS 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB  25 EDDNNHHHGHSKSGCVRCEDEPRMHPRCLEQCREEERERKQERSRHREADRSGEGSS 84
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RESULT 4
O9S6Z6
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```
ID  09S6Z6          PRELIMINARY;      PRT;      238 AA.
AC  09S6Z6;
DT  01-MAY-2000 (TREMBLrel. 13, Created)
DT  01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT  01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE  GLOBULIN-1 (FRAGMENT).
OS  Zea luxurians (Teosinte).
OC  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC  Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX  NCBI_TaxId=15945;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  Hilton H., Gaut B.S.;
RT  "Speciation and domestication in maize and its wild relatives:
RT  evidence from the globulin-1 gene.";
RL  Genetics 0:0-0(1998).
DR  EMBL; AF064232; AAC31475.1; -.
DR  EMBL; AF064227; AAC31470.1; -.
DR  EMBL; AF064230; AAC31473.1; -.
DR  HSSP; P50477; ICAU.
DR  INTERPRO; IPR000901; -.
DR  INTERPRO; IPR001113; -.
DR  PFAM; PF00546; Seedstore_7s; 1.
DR  PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
FT  NON_TER 238
SQ  SEQUENCE 238 AA; 27271 MW; FFE2169616319268 CRC64;
```

```
Query Match          98.9%; Score 346; DB 10; Length 238;
Best Local Similarity 98.3%; Pred. No. 1.6e-31;
Matches 59; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
OY  1 EDDNNHHHGHSKSGCVRCEDEPRMHPRCLEQCREEERERKQERSRHREADRSGEGSS 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB  25 EDDNNHHHGHSKSGCVRCEDEPRMHPRCLEQCREEERERKQERSRHREADRSGEGSS 84
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```
RESULT 5
ID  081252          PRELIMINARY;      PRT;      240 AA.
AC  081252;
DT  01-NOV-1998 (TREMBLrel. 08, Created)
DT  01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT  01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE  GLOBULIN-1 (FRAGMENT).
OS  Zea mays subsp. mays (maize).
OC  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC  Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX  NCBI_TaxId=4578;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  Hilton H., Gaut B.S.;
RT  "Speciation and domestication in maize and its wild relatives:
RT  evidence from the globulin-1 gene.";
RL  Genetics 0:0-0(1998).
DR  EMBL; AF064215; AAC31458.1; -.
DR  HSSP; P50477; ICAU.
DR  MENDEL; 31894; Zeama:1188;31894.
DR  INTERPRO; IPR000901; -.
DR  INTERPRO; IPR001113; -.
DR  PFAM; PF00546; Seedstore_7s; 1.
DR  PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
FT  NON_TER 240
SQ  SEQUENCE 240 AA; 27560 MW; 5F54BC5CB06A983D CRC64;
```

```
Query Match          98.9%; Score 346; DB 10; Length 240;
Best Local Similarity 98.3%; Pred. No. 1.7e-31;
Matches 59; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
OY  1 EDDNNHHHGHSKSGCVRCEDEPRMHPRCLEQCREEERERKQERSRHREADRSGEGSS 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB  25 EDDNNHHHGHSKSGCVRCEDEPRMHPRCLEQCREEERERKQERSRHREADRSGEGSS 84
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RESULT 6
ID 003866 PRELIMINARY: PRT: 540 AA.
AC 003866.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN-LIKE EMBRYO STORAGE PROTEIN.
GN GLI1-S.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OC NCBI_TaxID=4577;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=VA26;
RX MEDLINE=92090707; PubMed=1752424;
RA Belanger F.C., Kriz A.L.;
RT "Molecular basis for allelic polymorphism of the maize Globulin-1
   gene.";
RL Genetics 129:863-872(1991).
DR EMBL: X59084; CAA41810.1; -.
DR HSSP: P02853; 2PHL.
DR MENDEL: 11235; Zeama; 1188; 11235.
DR INTERPRO: IPR000901; -.
DR PFAM: PF00546; Seedstore_7s; 2.
DR PROSITE: PS00867; CPSASE_2; UNKNOWN_1.
DR PRODOR: PD081059; -. 1.
KW Seed storage protein.
SQ SEQUENCE 540 AA; 60239 MW; 7E1E918CF9C81993 CRC64;

Query Match 98.9%; Score 346; DB 10; Length 540;
Best Local Similarity 98.3%; Pred. No. 3.2e-31;
Matches 59; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDDNNHHHGKSGQVCVRCEDRPMHQRPRCLDCCREERERKROERSRHHEDDRSGGSS 60
   |||||||
Db 25 EDDNNHHHGKSGQVCVRCEDRPMHQRPRCLDCCREERERKROERSRHHEDDRSGGSS 84

RESULT 7
ID 081249 PRELIMINARY: PRT: 238 AA.
AC 081249.
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GLOBULIN-1 (FRAGMENT).
OS Zea mays subsp. mays (maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OC NCBI_TaxID=4578;
RN 11
RP SEQUENCE FROM N.A.
RA Hilton H., Gaut B.S.;
RT "Speciation and domestication in maize and its wild relatives:
   evidence from the globulin-1 gene.";
RL Genetics 0:0-0(1998).
DR EMBL: AF064212; AAC31455.1; -.
DR HSSP: P50477; ICAU.
DR MENDEL: 31891; Zeama; 1188; 31891.
DR INTERPRO: IPR000901; -.
DR PFAM: PF00546; Seedstore_7s; 1.
DR PROSITE: PS00867; CPSASE_2; UNKNOWN_1.
FT NON_TER 238
SQ SEQUENCE 238 AA; 27298 MW; EDF6A1DE3F66D0F0 CRC64;

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Query Match 97.7%; Score 342; DB 10; Length 238;
Best Local Similarity 96.7%; Pred. No. 4.6e-31;
Matches 58; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDDNNHHHGKSGQVCVRCEDRPMHQRPRCLDCCREERERKROERSRHHEDDRSGGSS 60
   |||||||
Db 25 EDDNNHHHGKSGQVCVRCEDRPMHQRPRCLDCCREERERKROERSRHHEDDRSGGSS 84

RESULT 8
ID 081255 PRELIMINARY: PRT: 238 AA.
AC 081255.
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE GLOBULIN-1 (FRAGMENT).
OS Zea mays subsp. parviglumis.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OC NCBI_TaxID=76912;
RN 11
RP SEQUENCE FROM N.A.
RA Hilton H., Gaut B.S.;
RT "Speciation and domestication in maize and its wild relatives:
   evidence from the globulin-1 gene.";
RL Genetics 0:0-0(1998).
DR EMBL: AF064224; AAC31467.1; -.
DR MENDEL: 31897; Zeama; 1188; 31897.
DR INTERPRO: IPR000901; -.
DR PFAM: PF00546; Seedstore_7s; 1.
DR PROSITE: PS00867; CPSASE_2; UNKNOWN_1.
FT NON_TER 238
SQ SEQUENCE 238 AA; 27205 MW; 1186EA5D6EBB507E CRC64;

Query Match 97.7%; Score 342; DB 10; Length 238;
Best Local Similarity 96.7%; Pred. No. 4.6e-31;
Matches 58; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDDNNHHHGKSGQVCVRCEDRPMHQRPRCLDCCREERERKROERSRHHEDDRSGGSS 60
   |||||||
Db 25 EDDNNHHHGKSGQVCVRCEDRPMHQRPRCLDCCREERERKROERSRHHEDDRSGGSS 84

RESULT 9
ID 09SBEB PRELIMINARY: PRT: 238 AA.
AC 09SBEB.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GLOBULIN-1 (FRAGMENT).
OS Zea mays subsp. parviglumis.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OC NCBI_TaxID=76912;
RN 11
RP SEQUENCE FROM N.A.
RA Hilton H., Gaut B.S.;
RT "Speciation and domestication in maize and its wild relatives:
   evidence from the globulin-1 gene.";
RL Genetics 0:0-0(1998).
DR EMBL: AF064221; AAC31464.1; -.
DR HSSP: P50477; ICAU.
DR INTERPRO: IPR000901; -.
DR PFAM: PF00546; Seedstore_7s; 1.
DR PROSITE: PS00867; CPSASE_2; UNKNOWN_1.
FT NON_TER 238
SQ SEQUENCE 238 AA; 27362 MW; A75C0C7DED9B773A CRC64;

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Query Match 97.7%; Score 342; DB 10; Length 238;
Best Local Similarity 96.7%; Pred. No. 4.6e-31;
Matches 58; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDDNNHHNGHKGSGQCYRCEDRPWHORPRLCQCREEEREKKOERSRHHADDSGSGSS 60
|||||
DB 25 EDDNNHHNGHKGSGQCYRCEDRPWHORPRLCQCREEEREKKOERSRHHADDSGSGSS 84

RESULT 10

Q9SBF0 PRELIMINARY; PRT; 240 AA.
ID Q9SBF0
AC Q9SBF0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE GLOBULIN-1 (FRAGMENT).
OS Zea mays subsp. parviglumis.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RA Hillon H., Gaut B.S.;
RT "Speciation and domestication in maize and its wild relatives:
evidence from the Globulin-1 gene.";
RL Genetics 0:0-0(1998).
DR EMBL: AF064219; AAC31462.1; -.
DR HSSP: P50477; ICAU.
DR INTERPRO: IPR000901; -.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
DR PROSITE: PS00867; CPSASE_2; UNKNOWN_1.
FT NON_TER 240
SQ SEQUENCE 240 AA; 27499 MW; ECDEL3393DC94AAC CRC64;

Query Match 97.7%; Score 342; DB 10; Length 240;
Best Local Similarity 96.7%; Pred. No. 4.6e-31;
Matches 58; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDDNNHHNGHKGSGQCYRCEDRPWHORPRLCQCREEEREKKOERSRHHADDSGSGSS 60
|||||
DB 25 EDDNNHHNGHKGSGQCYRCEDRPWHORPRLCQCREEEREKKOERSRHHADDSGSGSS 84

RESULT 11

Q9SBE9 PRELIMINARY; PRT; 240 AA.
ID Q9SBE9
AC Q9SBE9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE GLOBULIN-1 (FRAGMENT).
OS Zea mays subsp. parviglumis.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RA Hillon H., Gaut B.S.;
RT "Speciation and domestication in maize and its wild relatives:
evidence from the Globulin-1 gene.";
RL Genetics 0:0-0(1998).
DR EMBL: AF064220; AAC31463.1; -.
DR HSSP: P50477; ICAU.
DR INTERPRO: IPR000901; -.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
DR PROSITE: PS00867; CPSASE_2; UNKNOWN_1.
FT NON_TER 240
SQ SEQUENCE 240 AA; 27492 MW; ECC26326633DFFB9 CRC64;

Query Match 97.7%; Score 342; DB 10; Length 240;
Best Local Similarity 96.7%; Pred. No. 4.6e-31;
Matches 58; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDDNNHHNGHKGSGQCYRCEDRPWHORPRLCQCREEEREKKOERSRHHADDSGSGSS 60
|||||
DB 25 EDDNNHHNGHKGSGQCYRCEDRPWHORPRLCQCREEEREKKOERSRHHADDSGSGSS 84

RESULT 12

Q9SBE7 PRELIMINARY; PRT; 240 AA.
ID Q9SBE7
AC Q9SBE7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE GLOBULIN-1 (FRAGMENT).
OS Zea mays subsp. parviglumis.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RA Hillon H., Gaut B.S.;
RT "Speciation and domestication in maize and its wild relatives:
evidence from the Globulin-1 gene.";
RL Genetics 0:0-0(1998).
DR EMBL: AF064223; AAC31466.1; -.
DR HSSP: P50477; ICAU.
DR INTERPRO: IPR000901; -.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
DR PROSITE: PS00867; CPSASE_2; UNKNOWN_1.
FT NON_TER 240
SQ SEQUENCE 240 AA; 27604 MW; 2E0A2A2944B537DB CRC64;

Query Match 97.7%; Score 342; DB 10; Length 240;
Best Local Similarity 96.7%; Pred. No. 4.6e-31;
Matches 58; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDNNHHNGHKGSGQCYRCEDRPWHORPRLCQCREEEREKKOERSRHHADDSGSGSS 60
|||||
DB 25 EDDNNHHNGHKGSGQCYRCEDRPWHORPRLCQCREEEREKKOERSRHHADDSGSGSS 84

RESULT 13

Q41750 PRELIMINARY; PRT; 407 AA.
ID Q41750
AC Q41750;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE GLOBULIN1.
GN GUB1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-IHP, ILLINOIS HIGH PROTEIN;
RA Bhatramakki D., Kriz A.L.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U28017; AAB60295.1; -.
DR MENDEL: 11236; zeama; 1188; 11236.
DR INTERPRO: IPR000901; -.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
DR PROSITE: PS00867; CPSASE_2; UNKNOWN_1.
FT NON_TER 407
SQ SEQUENCE 407 AA; 46684 MW; 285E3ADE3C22969F CRC64;

Query Match 97.7%; Score 342; DB 10; Length 407;
 Best Local Similarity 96.7%; Pred. No. 7.2e-31;
 Matches 58; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDDNNHHGKSGCVCRCEDRPWHQRPCLCQCREEERERKROERSRHEADDRSGEGSS 60
 |||
 DB 25 EDDNNHHGKSGCVCRCEDRPWHQRPCLCQCREEERERKROERSRHEADDRSGEGSS 84

RESULT 14

081258 PRELIMINARY; PRT; 238 AA.

AC 081258;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE GLOBULIN-1 (FRAGMENT).
 OS Zea luxurians (Teosinte).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
 OX NCBI_TaxID=15945;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hilton H., Gaut B.S.;
 RT "Speciation and domestication in maize and its wild relatives:
 evidence from the globulin-1 gene."
 RL Genetics 0:0-0(1998).
 DR EMBL; AF064229; AAC31472.1; -.
 DR HSSP; P50477; ICAU.
 DR MENDEL; 31900; Zealu:1188; 31900.
 DR INTERPRO; IPR001113; -.
 DR PFAM; PF00546; Seedstore_7s; 1.
 FT NON_TER 238
 SO SEQUENCE 238 AA; 27306 MW; BCA3CB36FB28C6E2 CRC64;

Query Match 97.4%; Score 341; DB 10; Length 238;
 Best Local Similarity 96.7%; Pred. No. 6e-31;
 Matches 58; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDNNHHGKSGCVCRCEDRPWHQRPCLCQCREEERERKROERSRHEADDRSGEGSS 60
 |||
 DB 25 EDDNNHHGKSGCVCRCEDRPWHQRPCLCQCREEERERKROERSRHEADDRSGEGSS 84

RESULT 15

081256 PRELIMINARY; PRT; 240 AA.

AC 081256;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE GLOBULIN-1 (FRAGMENT).
 OS Zea mays subsp. parviglumis.
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
 OX NCBI_TaxID=76912;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hilton H., Gaut B.S.;
 RT "Speciation and domestication in maize and its wild relatives:
 evidence from the globulin-1 gene."
 RL Genetics 0:0-0(1998).
 DR EMBL; AF064226; AAC31469.1; -.
 DR HSSP; P50477; ICAU.
 DR MENDEL; 31898; Zeama:1188; 31898.
 DR INTERPRO; IPR000901; -.
 DR PFAM; PF00546; Seedstore_7s; 1.
 DR PROSITE; PS00867; CPBASE_2; UNKNOWN_1.
 FT NON_TER 240
 SO SEQUENCE 240 AA; 27457 MW; CCC2E1CEDA04D9B1 CRC64;

SO SEQUENCE 240 AA; 27457 MW; CCC2E1CEDA04D9B1 CRC64;

Query Match 97.1%; Score 340; DB 10; Length 240;
 Best Local Similarity 96.7%; Pred. No. 7.8e-31;
 Matches 58; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDNNHHGKSGCVCRCEDRPWHQRPCLCQCREEERERKROERSRHEADDRSGEGSS 60
 |||
 DB 25 EDDNNHHGKSGCVCRCEDRPWHQRPCLCQCREEERERKROERSRHEADDRSGEGSS 84

Search completed: March 1, 2001, 16:17:16
 Job time: 454 sec

